



Patent  
Attorney Docket: 266/187

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re the Application of:

Neil H. Bander

Serial No.: 09/929,665

Filed: July 20, 1999

(Continuation of S.N. 09/357,704 (242/024))

For: TREATMENT AND DIAGNOSIS OF  
PROSTATE CANCER

)  
) **Group Art Unit: 1642**

)  
) **Examiner: Not yet assigned**

TRANSMITTAL OF SUBSTITUTE DRAWINGS UNDER 37 CFR 1.84

Commissioner for Patents  
Washington, D.C. 20231

Sir:

In response to a Notice to File Corrected Application Papers, Applicant transmits herewith substitute drawings (11 sheets) in compliance with the requirements of 37 CFR 1.84. These drawings are deemed formal drawings and are identical to those previously submitted in the parent U.S. Patent Application Serial No. 09/357,704.

No fee is deemed necessary in the filing of the substitute drawings. However, should a fee be deemed necessary, the Commissioner is authorized and requested to charge any amounts due on

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(37 C.F.R. §1.8a)

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Felicia Reyes

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*Felicia Reyes*

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account of the present submission to the Deposit Account of the undersigned attorneys, which is:  
**Deposit Account No. 12-2475.**

Respectfully submitted,  
LYON & LYON LLP

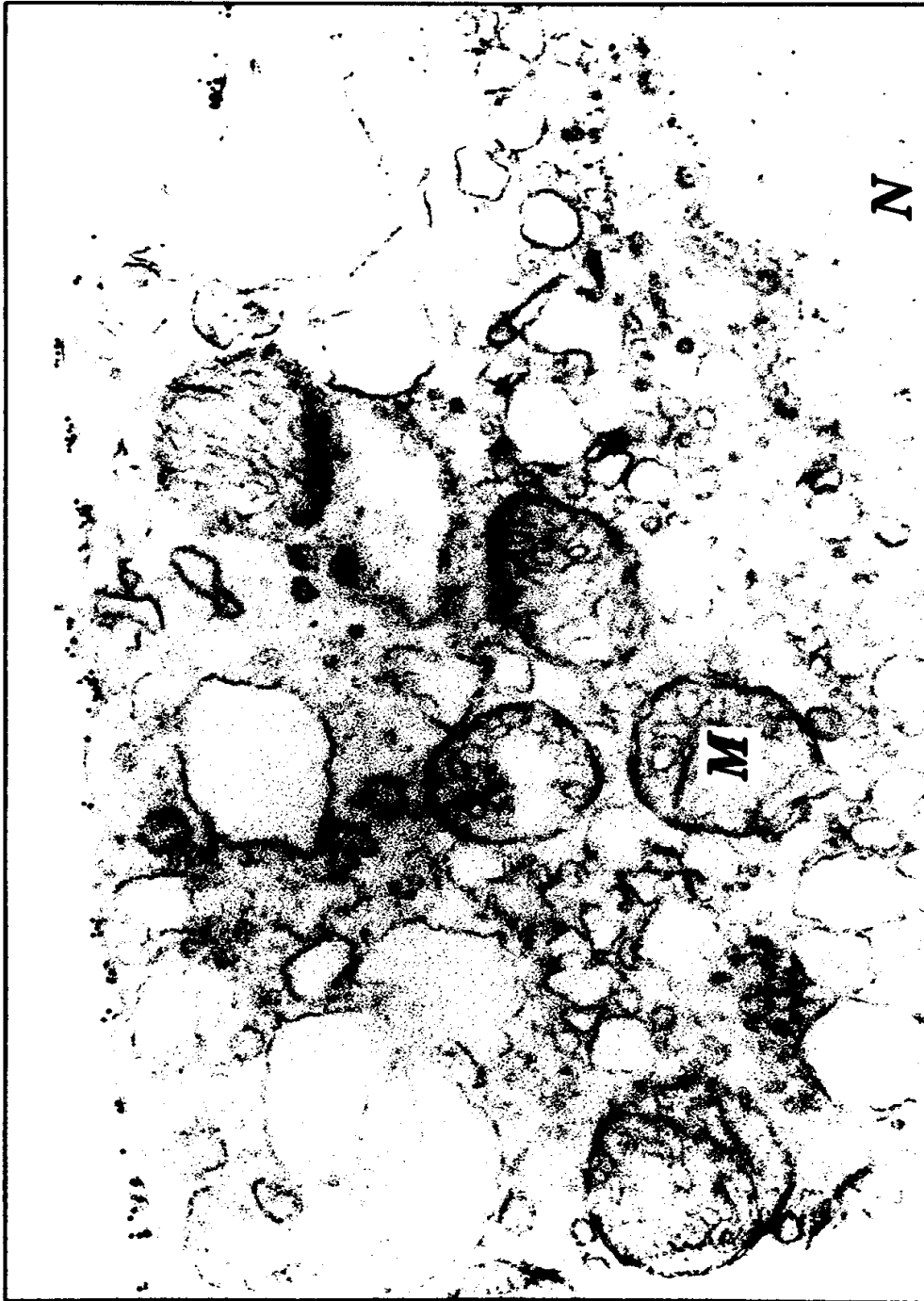
Dated: October 25, 2001

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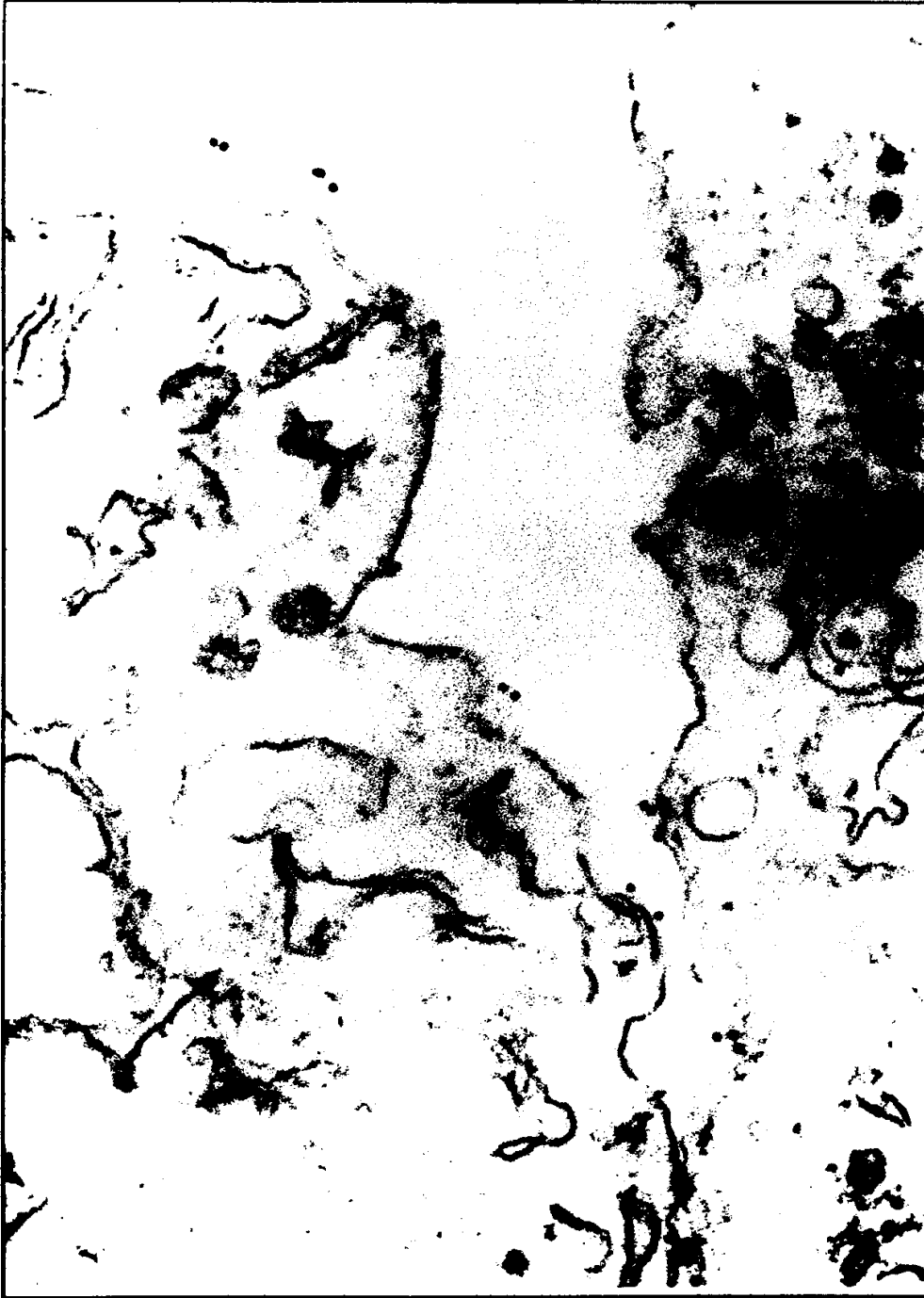
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***FIG. 1***

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T0702T" 59962660

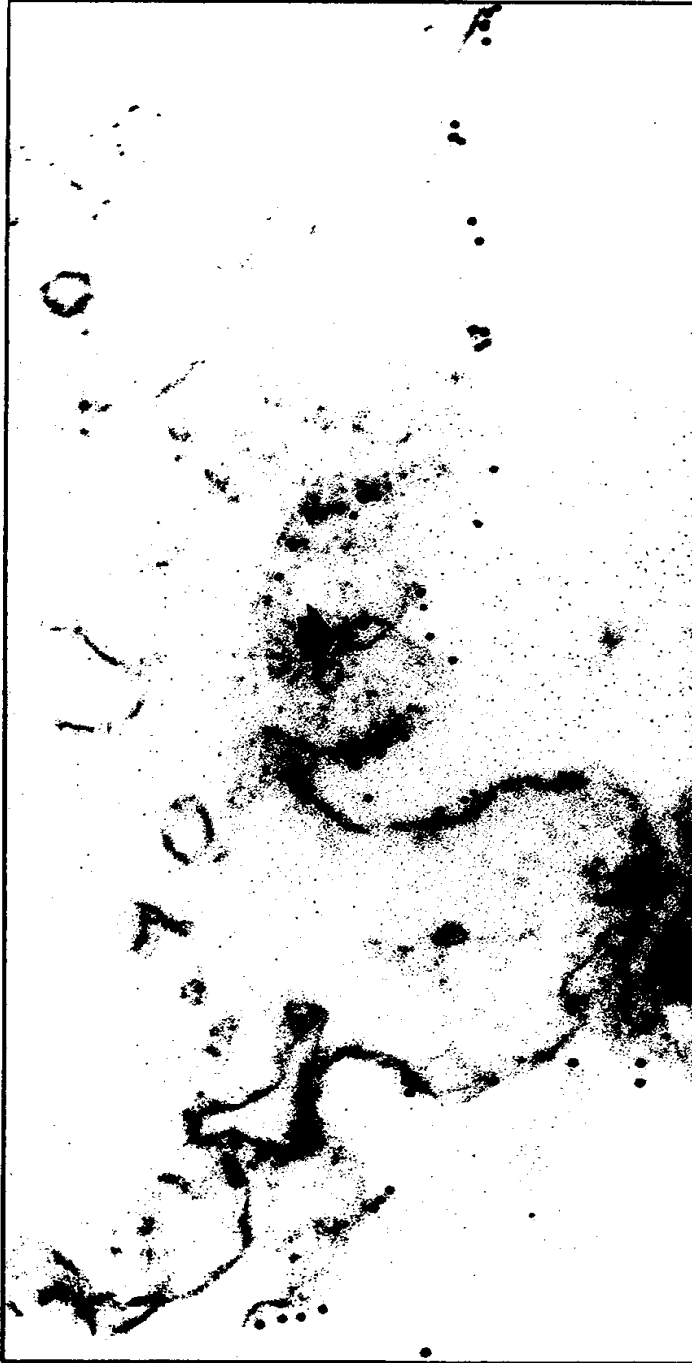
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**FIG. 2**

09/929,665-120701

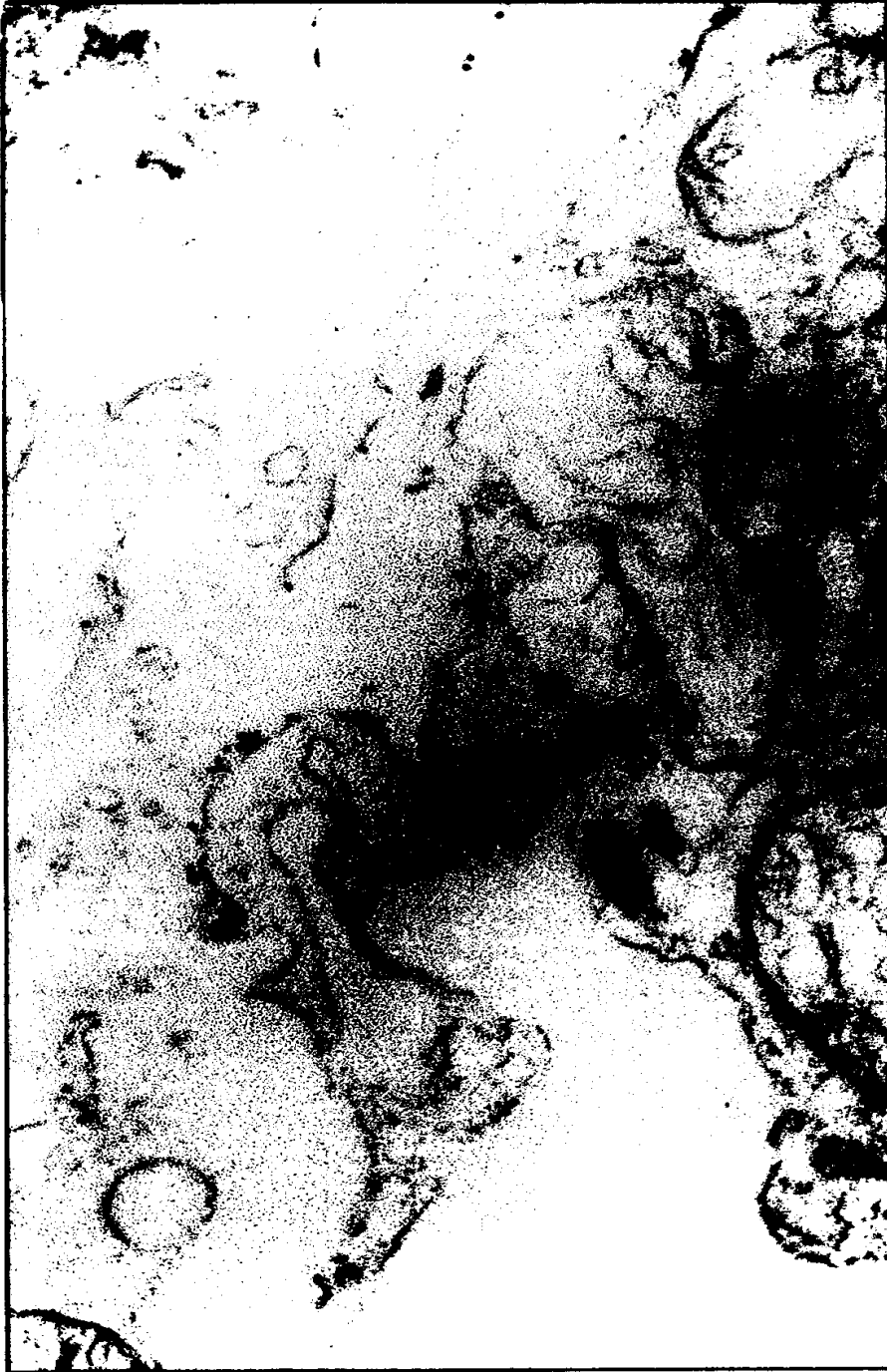
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**FIG. 3**

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**FIG. 4**

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**FIG. 5**

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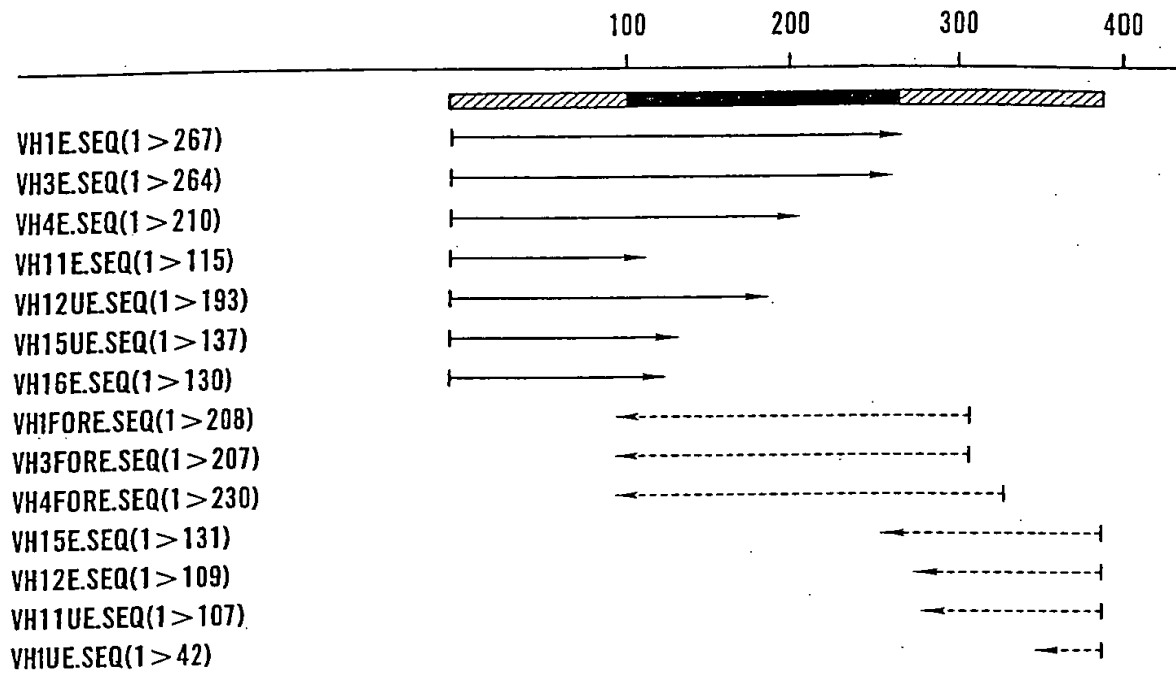


FIG. 6



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ENZYMES: ALL 74 ENZYMES (NO FILTER)

SETTINGS: LINEAR, CERTAIN SITES ONLY, STANDARD GENETIC CODE

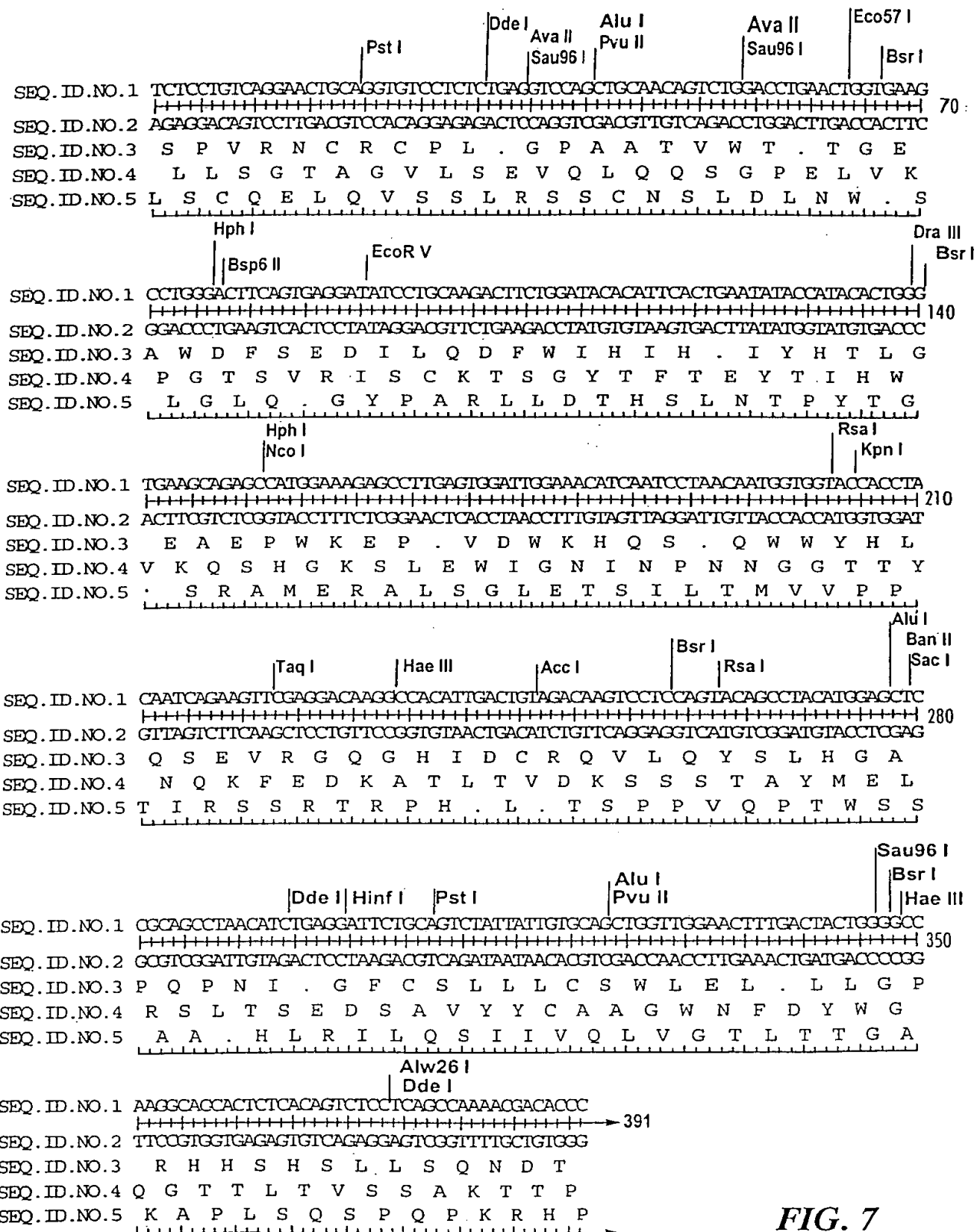


FIG. 7

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LIPMAN-PEARSON PROTEIN ALIGNMENT  
 KTUPLE: 2; GAP PENALTY: 4; GAP LENGTH PENALTY: 12

SEQ1(1>115) J591VH.PRO	SEQ2(1>125) MUVHIIA.PRO	SIMILARITY INDEX	GAP NUMBER	GAP LENGTH	CONSENSUS LENGTH
(1>115)	(1>125)	75.6	2	10	125

EVQLQQSGPELVKPGTSVRI SCKTSGYTFTEYTI -HWVKQSHGKSLEWIGNINPNNGGTT  
 EVQLQQSGPELVKPG:SV:ISCK:SGYTFT:Y : :WVKQS.GKSLEWIG:INP.NGGT:  
 EVQLQQSGPELVKPGASVKISCKASGYTFTDYIMNHWVKQSPGKSLEWIGDINPGNGGTS  
 YNQKFEDKATLTIVDKSSSTAYMELRSLTSEDSAVYYCAAG-----WNFDYWGGGTT  
 YNQKF.:KATLTIVDKSSSTAYM:L.SLTSEDSAVYYCA G ..FDYWGGGTT  
 YNQKFKGKATLTIVDKSSSTAYMQLSLTSEDSAVYYCARGYSSSYMAYYAFDYWGQGIT  
 10 20 30 40 50 60 70 80 90 100 110 120

LTVSS

:TVSS

VTVSS

FIG. 8

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TREATMENT AND DIAGNOSIS OF PROSTATE CANCER

INV: N. BANDER

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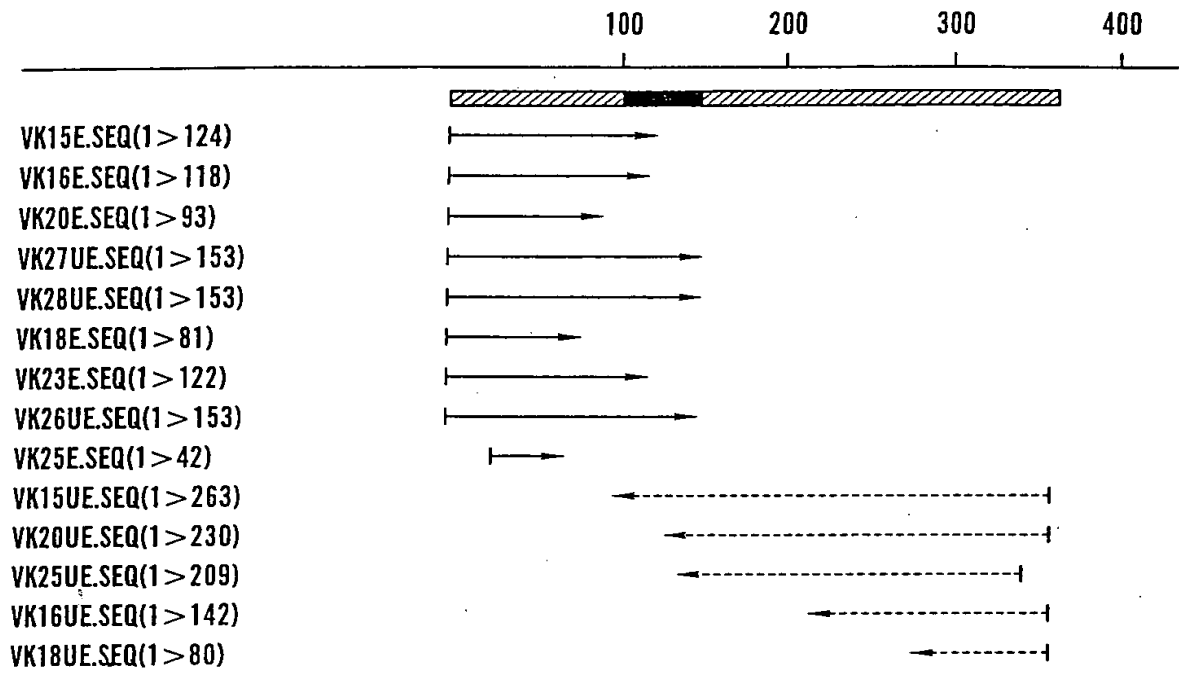


FIG. 9

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ENZYMES: ALL 74 ENZYMES (NO FILTER):  
 SETTINGS: LINEAR, CERTAIN SITES ONLY, STANDARD GENETIC CODE

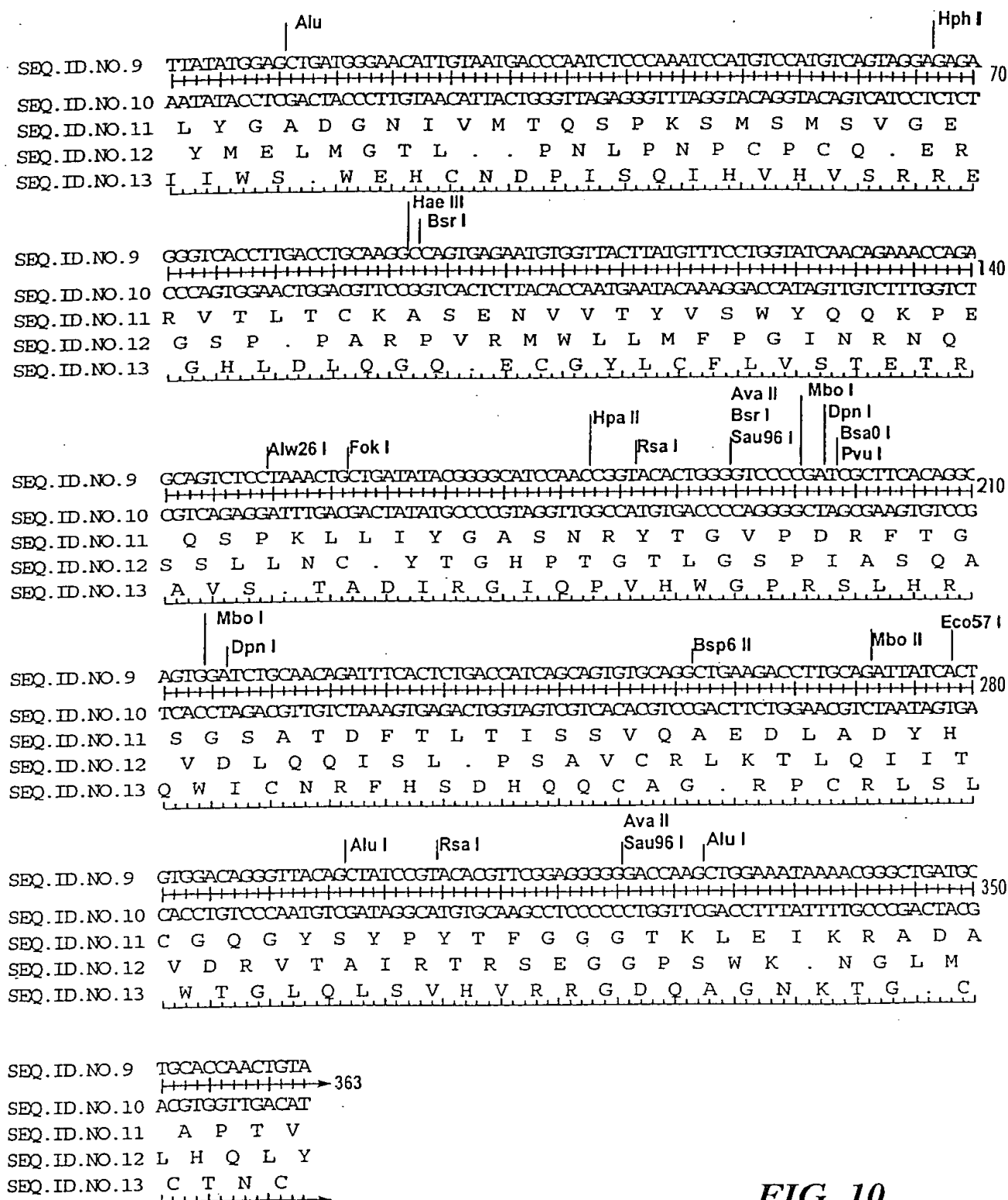


FIG. 10

[illegible]

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## LIPMAN-PEARSON PROTEIN ALIGNMENT

KTUPLE: 2; GAP PENALTY: 4; GAP LENGTH PENALTY: 12

SEQ1(1>107) J591VK.PRO	SEQ2(1 > 1 1 1) MUVKV.PRO	SIMILARITY INDEX	GAP NUMBER	GAP LENGTH	CONSENSUS LENGTH
(1>107)	(1>109)	60.4	2	2	109

↓10      ↓20      ↓30      ↓40      ↓50  
 NIVMTQSPKSMMSVGERVILTCKAS-ENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVP  
 :I MIQSP.S:S S:G:RVT:TC:AS ::: .Y::WYQQK. SPKLLIY AS. .:GVP  
 DIQMTQSPSSLSASLGDRVTITCRASQDDISNYLWYQQKPGGSPKLLIYYASRLHSGVP  
       ↑10      ↑20      ↑30      ↑40      ↑50      ↑60  
 ↓60      ↓70      ↓80      ↓90      ↓100  
 DRFTGSGSATDFTLTISVQAEDLADYHCGQGY-SY-PYTFGGGTKLEIK  
 .RF:GSGS:TD::LTIS:::ED:A.Y C QG : P TFGGGTKLEIK  
 SRFSGSGSGTDYSLTISNLEQEDIATYFQQGNILPPRTFGGGTKLEIK  
       ↑70      ↑80      ↑90      ↑100

FIG. 11

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